

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail-Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr.Link _____
Date Completed: <u>4/8</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

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GenCore version 5.1.4_p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2003, 23:47:29 ; Search time 83 Seconds
(without alignments)
6384.788 Million cell updates/sec

Title: US-09-847-081B-1

Perfect score: 1728

Sequence: 1 agaaaccagaagaacaac.....tcatcaaacctcaagtga 1728

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	868	50.2	1826	1	US-08-579-667-5	Sequence 5, Appl
2	858.6	49.7	1795	1	US-08-579-667-1	Sequence 1, Appl
3	853.4	49.4	1814	1	US-08-579-667-7	Sequence 7, Appl
4	842	48.7	1646	1	US-07-995-950-2	Sequence 2, Appl
5	842	48.7	1646	1	US-08-300-582-2	Sequence 2, Appl
6	811.2	46.9	1239	4	US-09-180-342-2	Sequence 2, Appl
7	811.2	46.9	1316	1	US-08-579-667-3	Sequence 3, Appl
8	415.2	24.0	1239	4	US-09-180-342-1	Sequence 1, Appl
9	172	10.0	749	1	US-08-579-667-9	Sequence 9, Appl
10	54	3.1	7218	1	US-08-232-463-14	Sequence 14, Appl
11	52.4	3.0	114	2	US-08-260-546-10	Sequence 10, Appl
12	52.4	3.0	114	4	US-09-436-068A-12	Sequence 12, Appl
13	37.2	2.2	891	1	US-07-783-705A-11	Sequence 11, Appl
14	37.2	2.2	1232	4	US-08-908-758-1	Sequence 1, Appl
15	37.2	2.2	6918	1	US-07-783-705A-13	Sequence 13, Appl
16	36	2.1	1959	3	US-09-166-460-1	Sequence 1, Appl
17	36	2.1	1959	4	US-09-361-718-1	Sequence 1, Appl
18	36	2.1	1959	4	US-09-398-395A-27	Sequence 27, Appl
19	35.4	2.0	2468	1	US-08-468-036-19	Sequence 19, Appl
20	35.4	2.0	2468	2	US-08-376-843-19	Sequence 19, Appl
21	35.4	2.0	2469	1	US-08-447-500-3	Sequence 3, Appl
22	35.4	2.0	2469	1	US-08-454-097-3	Sequence 3, Appl
23	35.4	2.0	2469	1	US-08-453-866-3	Sequence 3, Appl
24	35.4	2.0	2469	3	US-08-185-359-3	Sequence 3, Appl
25	34.8	2.0	654	4	US-09-288-143-37	Sequence 37, Appl
26	34	2.0	1056	4	US-09-134-001C-2655	Sequence 2655, Ap
27	33.4	1.9	25002	4	US-08-961-527-48	Sequence 48, Appl

28	33.2	1.9	18475	4	US-08-961-527-38	Sequence 38, Appl
29	33	1.9	6265	4	US-09-129-112-3	Sequence 3, Appl
30	33	1.9	98844	4	US-09-791-211-10	Sequence 10, Appl
31	32.8	1.9	1923	4	US-09-149-476-192	Sequence 192, App
32	32.8	1.9	1988	4	US-09-643-597-173	Sequence 173, App
33	32.8	1.9	12734	4	US-09-344-456-1	Sequence 1, Appl
34	32.8	1.9	14078	4	US-09-433-262-1	Sequence 1, Appl
35	32.8	1.9	14078	4	US-09-702-330-1	Sequence 1, Appl
36	32.6	1.9	14578	3	US-08-859-694-1	Sequence 1, Appl
37	32.6	1.9	363	2	US-08-967-101-30	Sequence 30, Appl
38	32.6	1.9	363	2	US-08-592-541-30	Sequence 30, Appl
39	32.6	1.9	363	3	US-09-124-698-30	Sequence 30, Appl
40	32.6	1.9	363	3	US-09-127-480-30	Sequence 30, Appl
41	32.6	1.9	363	4	US-08-496-841C-30	Sequence 30, Appl
42	32.6	1.9	363	4	US-09-124-523-30	Sequence 30, Appl
43	32.6	1.9	1449	4	US-08-858-207A-54	Sequence 54, Appl
44	32.6	1.9	5910	4	US-08-961-527-165	Sequence 165, App
45	32.6	1.9	28882	4	US-08-961-527-140	Sequence 140, App

ALIGNMENTS

RESULT 1

US-08-579-667-5

Sequence 5, Application US/08579667

Patent No. 5705624

GENERAL INFORMATION:

APPLICANT: Fitzmaurice, Wayne P.

APPLICANT: Hellmann, Gary M.

APPLICANT: Grill, Laurence K.

APPLICANT: Kumagai, Monto H.

APPLICANT: Della-Cioppa, Guy R.

TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN

TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Virginia C. Bennett

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COUNTRY: USA

ZIP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: US/08/579,667

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

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REGISTRATION NUMBER: 37,092

REFERENCE/DOCKET NUMBER: 627-196

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-420-2200

TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1826 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 367..1596

US-08-579-667-5

Query Match 50.2%; Score 868; DB 1; Length 1826;

Best Local Similarity 77.2%; Pred. No. 3.8e-239;

